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      Wenger, Kevin S
      Bisgard-Frantzen, Henrik
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550 555 560

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Ser Glu Gly Ala Tyr Ser Gly Ile Val Ile Ala Ser Pro Ser Lys Thr 35 40 45

Ser Pro Asp Tyr Leu Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe 50 55 60

Lys Met Leu Ile Asp Gln Tyr Thr Asn Gly Leu Asp Thr Thr Leu Arg

Thr Leu Ile Asp Glu Phe Val Ser Ala Glu Ala Thr Ile Gln Gln Thr 80 85 90

Ser Asn Pro Ser Gly Thr Val Ser Thr Gly Gly Leu Gly Glu Pro Lys 95 100 105 110

Phe Asn Ile Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly Arg Pro Gln 115 120 125

Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Ile Met Thr Tyr Ala Thr 130 135 140

Tyr Leu Tyr Asn Asn Gly Asn Thr Ser Tyr Val Thr Asn Thr Leu Trp 145 150 155

- Pro Ile Ile Lys Leu Asp Leu Asp Tyr Val Asn Ser Asp Trp Asn Gln 160 165 170
- Thr Thr Phe Asp Leu Trp Glu Glu Val Asp Ser Ser Ser Phe Phe Thr 175 180 185 190
- Thr Ala Val Gln His Arg Ala Leu Val Gln Gly Ala Ala Phe Ala Thr 195 200 205
- Leu Ile Gly Gln Thr Ser Ser Ala Ser Thr Tyr Ser Ala Thr Ala Pro 210 215 220
- Ser Ile Leu Cys Phe Leu Gln Ser Tyr Trp Asn Thr Asn Gly Tyr Trp 225 230 235
- Thr Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Ile 240 245 250
- Leu Ala Ser Ile His Thr Phe Asp Ala Ser Ala Gly Cys Ser Ala Ala 255 260 265 270
- Thr Ser Gln Pro Cys Ser Asp Val Ala Leu Ala Asn Leu Lys Val Tyr 275 280 285
- Val Asp Ser Phe Arg Ser Ile Tyr Thr Ile Asn Ser Gly Ile Ser Ser 290 295 300
- Thr Ser Gly Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Tyr Asn 305 310 315
- Gly Asn Pro Trp Tyr Leu Cys Thr Leu Ala Val Ala Glu Gln Leu Tyr 320 325 330
- Asp Ala Leu Ile Val Trp Lys Ala Ala Gly Glu Leu Asn Val Thr Ser 335 340 345
- Val Ser Leu Ala Phe Phe Gln Gln Phe Asp Ser Ser Ile Thr Ala Gly 355 360 365
- Thr Tyr Ala Ser Ser Ser Ser Val Tyr Thr Ser Leu Ile Ser Asp Ile 370 375 380
- Gln Ala Phe Ala Asp Glu Phe Val Asp Ile Val Ala Lys Tyr Thr Pro 385 390 395

Ser Ser Gly Phe Leu Ser Glu Gln Tyr Asp Lys Ser Thr Gly Ala Gln 400 405 410

Asp Ser Ala Ala Asn Leu Thr Trp Ser Tyr Ala Ala Ala Ile Thr Ala 415 420 425 430

Tyr Gln Ala Arg Asn Gly Phe Thr Gly Ala Ser Trp Gly Ala Lys Gly 435 440 445

Val Ser Thr Ser Cys Ser Thr Gly Ala Thr Ser Pro Gly Gly Ser Ser 450 455 460

Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly
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Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr 480 485 490

Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser 495 500 505 510

Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val
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- Leu Asp Tyr Ile Glu Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro 50 55 60
- Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His 70 75 80
- Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr 85 90 95
- Ala Asp Asn Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
 100 105 110
- Tyr Leu Met Val Asp Val Val Pro Asp His Met Gly Tyr Ala Gly Asn 115 120 125
- Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser 130 135 140
- Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met 145 150 155 160
- Val Glu Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175
- Asp Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190
- Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205
- Leu Glu Val Gln Pro Asp Phe Phe Pro Gly Tyr Asn Lys Ala Ser Gly 210 215
- Val Tyr Cys Val Gly Glu Ile Asp Asn Gly Asn Pro Ala Ser Asp Cys 225 230 230 235
- Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp 245 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu 260 265 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Lys Tyr 290 295 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ala 325 330 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile 355 360 365

Arg Lys Leu Ala Ile Ala Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Ala Lys Gly Thr 385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr 420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser 435 440 445

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Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu

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- Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
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- Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
- Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn 210 215 220
- Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro 225 230 235
- Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr 240 245 250
- Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser 255 260 265
- Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro 270 275 280 285
- Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg 290 295 300
- Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala 305 310 315
- Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
- Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
- Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser 350 365
- Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
- Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met 385 390 395

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
400 405 410

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr 415 420 425

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr 430 435 440 445

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Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn 85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr 100 105 110

- Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val 115 120 125
- Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro 130 135 140
- Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 145 150 155 160
- Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175
- Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190
- Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205
- Ala Ala Glu Ile Lýs Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220
- Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 225 230 240
- Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 245 250 255
- Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 260 265 270
- Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285
- His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 290 295 300
- Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser 305 310 315
- Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His 385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp 405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr 435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser 450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr 465 470 475 480

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 50 .. 55 60
- Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu 70 75 80
- Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr 85 90 95
- Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
- Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser 115 120 125
- Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg 130 135 140
- Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160
- Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg 165 170 175
- Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn 180 185 190
- Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val 195 200 205
- Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser 210 215 220
- Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe 225 230 235 240
- Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met 245 250 255
- Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn 260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu 275 280 285

- His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Tyr Asp Met 290 295 300
- Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala 305 310 315 320
- Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335
- Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350
- Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365
- Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile 370 375 380
- Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His 385 390 395
- Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp 405 410 415
- Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430
- Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr 435 440 445
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Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp 50 60

Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr 65 70 75 80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met 85 90 95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly 100 105 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln 115 120 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe 130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His 145 150 155 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr 165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu 180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His 195 200 205

Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn 210 215 220

- Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys 225 230 235 240
- Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly 245 250 255
- Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys 260 265 270
- Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp 275 280 285
- Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr 290 295 300
- Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro 305 310 315
- Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln 325 330 335
- Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala 340 345 350
- Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp 355 360 365
- Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile 370 375 380
- Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His 385 390 395 400
- Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val 405 410 415
- Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430
- Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val 435 440 445
- Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser 450 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp 475 465 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr 490 485 Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val 510 505 Ala Trp <210> 8 <211> 38 <212> PRT <213> Aspergillus niger <220> <221> MISC_FEATURE <222> (1)..(38) <223> linker sequence <400> 8 Thr Gly Gly Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val 10 Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser 25 20 Thr Ser Ser Thr Ser Ala 35 <210> 9 <211> 31 <212> PRT <213> Aspergillus kawachi <220> <221> MISC_FEATURE <222> (1)..(31) <223> linker sequence <400> 9 Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr

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  Thr Ser Thr Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ala Ala
                                       10
                  5
  gct act act tct tca tca tgc acc gca aca agc acc acc ctc ccc atc
                                                                          96
  Ala Thr Thr Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile
              20
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acc Thr	ttc Phe	gaa Glu 35	gaa Glu	ctc Leu	gtc Val	acc Thr	act Thr 40	acc Thr	tac Tyr	Gly ggg	gaa Glu	gaa Glu 45	gtc Val	tac Tyr	ctc Leu	144	
agc Ser	gga Gly 50	tct Ser	atc Ile	tcc Ser	cag Gln	ctc Leu 55	gga Gly	gag Glu	tgg Trp	gat Asp	acg Thr 60	agt Ser	gac Asp	gcg Ala	gtg Val	192	
aag Lys 65	ttg Leu	tcc Ser	gcg Ala	gat Asp	gat Asp 70	tat Tyr	acc Thr	tcg Ser	agt Ser	aac Asn 75	ccc Pro	gag Glu	tgg Trp	tct Ser	gtt Val 80	240	
act Thr	gtg Val	tcg Ser	ttg Leu	ccg Pro 85	gtg Val	ggg Gly	acg Thr	acc Thr	ttc Phe 90	gag Glu	tat Tyr	aag Lys	ttt Phe	att Ile 95	aag Lys	288	
gtc Val	gat Asp	gag Glu	ggt Gly 100	gga Gly	agt Ser	gtg Val	act Thr	tgg Trp 105	gaa Glu	agt Ser	gat Asp	ccg Pro	aat Asn 110	agg Arg	gag Glu	336	-
tat Tyr	act Thr	gtg Val 115	cct Pro	gaa Glu	tgt Cys	GJÀ ààà	aat Asn 120	ggg Gly	agt Ser	GJ A .ddd	gag Glu	acg Thr 125	gtg Val	gtt Val	gat Asp	384	
	tgg Trp 130		tag													396	ò
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<40	0>	13															
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Ala	Thr	Ťhr	Ser 20	Ser	Ser	Cys	Thr	Ala 25	Thr	Ser	Thr	Thr	Leu 30	Pro	Ile		
Thr	Phe	Glu 35	Glu	Leu	Val	Thr	Thr 40	Thr	Туг	Gly	Glu	Glu 45	Val	Tyr	Leu		
Ser	Gly 50	Ser	· Ile	Ser	Gln	Беч 55	Gly	Glu	Trp	Asp	Thr 60	Ser	Asp	Ala	Val		
Lys 65	Leu	Ser	: Ala	Asp	Asp 70	Tyr	Thr	Ser	Ser	Asn 75	Pro	Glu	Trp	Ser	Val 80		
Thr	. Val	. Ser	Leu	Pro	val	. Gly	Thr	Thr	Phe 90	e Glu	туз	Lys	Phe	11∈ 95	Lys		

Val Asp Glu Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu
100 105 110

Tyr Thr Val Pro Glu Cys Gly Asn Gly Ser Gly Glu Thr Val Val Asp 115 120 125

Thr Trp Arg 130

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<212> PRT

<213> Bacillus flavothermus

<220>

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<222> (1)..(102)

<223> CBM

<400> 14

Ile Ser Thr Thr Ser Gln Ile Thr Phe Thr Val Asn Asn Ala Thr Thr

Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn Ile Ser Gln Leu Gly 20 25 30

Asn Trp Asp Pro Val His Ala Val Gln Met Thr Pro Ser Ser Tyr Pro

Thr Trp Thr Val Thr Ile Pro Leu Leu Gln Gly Gln Asn Ile Gln Phe 50 55 60

Lys Phe Ile Lys Lys Asp Ser Ala Gly Asn Val Ile Trp Glu Asp Ile 65 70 80

Ser Asn Arg Thr Tyr Thr Val Pro Thr Ala Ala Ser Gly Ala Tyr Thr

Ala Ser Trp Asn Val Pro 100

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<211> 99

<212> PRT

<213> Bacillus sp.

<220>

<221> MISC_FEATURE `

<222> (1)..(99)

<223> CBM

<400> 15

Thr Ser Asn Val Thr Phe Thr Val Asn Asn Ala Thr Thr Val Tyr Gly
1 5 10 15

Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu Gly Asn Trp Asn 20 25 30

Ile Ala Asn Ala Ile Gln Met Thr Pro Ser Ser Tyr Pro Thr Trp Lys
35 40 45

Thr Thr Val Ser Leu Pro Gln Gly Lys Ala Ile Glu Phe Lys Phe Ile 50 55 60

Lys Lys Asp Ser Ala Gly Asn Val Ile Trp Glu Asn Ile Ala Asn Arg 70 75 80

Thr Tyr Thr Val Pro Phe Ser Ser Thr Gly Ser Tyr Thr Ala Asn Trp 85 90 95

Asn Val Pro

<210> 16

<211> 102

<212> PRT

<213> Alcaliphilic Bacillus

<220>

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<222> (1)...(102)

<223> CBM

<400> 16

Thr Ser Thr Thr Ser Gln Ile Thr Phe Thr Val Asn Asn Ala Thr Thr 1 5 10 15

Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn Ile Ser Gln Leu Gly 20 25 30

Asn Trp Asp Pro Val Asn Ala Val Gln Met Thr Pro Ser Ser Tyr Pro
35 40 45

Thr Trp Val Val Thr Val Pro Leu Pro Gln Ser Gln Asn Ile Gln Phe 50 55 60

Lys Phe Ile Lys Lys Asp Gly Ser Gly Asn Val Ile Trp Glu Asn Ile 65 70 75 80

Ser Asn Arg Thr Tyr Thr Val Pro Thr Ala Ala Ser Gly Ala Tyr Thr 85 90 95

Ala Asn Trp Asn Val Pro 100

<210> 17

<211> 112

<212> PRT

<213> Hormoconis resinae

<220>

<221> MISC FEATURE

<222> (1)..(112)

<223> CBM

<400> 17

Cys Gln Val Ser Ile Thr Phe Asn Ile Asn Ala Thr Thr Tyr Tyr Gly
1 5 10 15

Glu Asn Leu Tyr Val Ile Gly Asn Ser Ser Asp Leu Gly Ala Trp Asn 20 25 30

Ile Ala Asp Ala Tyr Pro Leu Ser Ala Ser Ala Tyr Thr Gln Asp Arg 35 40 45

Pro Leu Trp Ser Ala Ala Ile Pro Leu Asn Ala Gly Glu Val Ile Ser 50 55 60

Tyr Gln Tyr Val Arg Gln Glu Asp Cys Asp Gln Pro Tyr Ile Tyr Glu

Thr Val Asn Arg Thr Leu Thr Val Pro Ala Cys Gly Gly Ala Ala Val 85 90 95

Thr Thr Asp Asp Ala Trp Met Gly Pro Val Gly Ser Ser Gly Asn Cys
100 105 110

<210> 18

<211> 95

<212> PRT

<213> Lentinula edodes

<220>

<221> MISC_FEATURE

<222> (1)..(95)

<223> CBM

<400> 18

Val Ser Val Thr Phe Asn Val Asp Ala Ser Thr Leu Glu Gly Gln Asn 1 5 10 15

Val Tyr Leu Thr Gly Ala Val Asp Ala Leu Glu Asp Trp Ser Thr Asp 20 25 30

Asn Ala Ile Leu Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Val Thr 35 40 45

Val Asp Leu Pro Gly Ser Thr Asp Val Gln Tyr Lys Tyr Ile Lys Lys 50 55 60

Asp Gly Ser Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Met Glu Ile 65 70 75 80

Thr Thr Pro Ala Asn Gly Thr Tyr Ala Thr Asn Asp Thr Trp Arg 85 90 95

<210> 19

<211> 107

<212> PRT

<213> Neurospora crassa

<220>

<221> MISC_FEATURE

<222> (1)..(107)

<223> CBM

<400> 19

Cys Ala Ala Asp His Glu Val Leu Val Thr Phe Asn Glu Lys Val Thr

Thr Ser Tyr Gly Gln Thr Val Lys Val Val Gly Ser Ile Ala Ala Leu 20 25 30

Gly Asn Trp Ala Pro Ala Ser Gly Val Thr Leu Ser Ala Lys Gln Tyr 35 40 45 Ser Ser Ser Asn Pro Leu Trp Ser Thr Thr Ile Ala Leu Pro Gln Gly 50 55 60

Thr Ser Phe Lys Tyr Lys Tyr Val Val Val Asn Ser Asp Gly Ser Val 65 70 . 75 80

Lys Trp Glu Asn Asp Pro Asp Arg Ser Tyr Ala Val Gly Thr Asp Cys 85 90 95

Ala Ser Thr Ala Thr Leu Asp Asp Thr Trp Arg
100 105

<210> 20

<211> 115

<212> PRT

<213> Talaromyces byssochlamydioides

<220>

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Thr Phe Asp Glu Ile Val Thr Thr Thr Tyr Gly Glu Thr Val Tyr Leu 20 25 30

Ser Gly Ser Ile Pro Ala Leu Gly Asn Trp Asp Thr Ser Ser Ala Ile 35 40 45

Ala Leu Ser Ala Val Asp Tyr Thr Ser Ser Asn Pro Leu Trp Tyr Val 50 55

Thr Val Asn Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe Phe Val

Gln Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser 85 90 95

Tyr Thr Val Pro Ala Asn Cys Gly Gln Thr Thr Ala Ile Ile Asp Asp 100 105 110

Ser Trp Gln 115 <210> 21 <211> 115 <212> PRT <213> Geosmithia cylindrospora <220> <221> MISC FEATURE <222> (1)..(115) <223> CBM <400> 21 Thr Ser Thr Gly Ser Ala Pro Cys Thr Thr Pro Thr Thr Val Ala Val 10 Thr Phe Asp Glu Ile Val Thr Thr Ser Tyr Gly Glu Thr Val Tyr Leu 20 Ala Gly Ser Ile Ala Ala Leu Gly Asn Trp Asp Thr Asn Ser Ala Ile 40 35 Ala Leu Ser Ala Ala Asp Tyr Thr Ser Asn Asn Leu Trp Tyr Val Thr Val Asn Leu Ala Ala Gly Thr Ser Phe Gln Tyr Lys Phe Phe Val 70 Lys Glu Thr Asp Ser Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala Asn Cys Gly Gln Thr Thr Ala Ile Ile Asp Asp 105 Thr Trp Gln 115 <210> 22 <211> 139 <212> PRT <213> Scorias spongiosa CBM <220> <221> MISC_FEATURE <222> (1)..(139) <223> CBM

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Ala Lys Val Pro Ser Thr Cys Ser Ala Ser Ser Ala Thr Gly Thr Cys
1 10 15

Thr Thr Ala Thr Ser Thr Phe Gly Gly Ser Thr Pro Thr Thr Ser Cys 25 30

Ala Thr Thr Pro Thr Leu Thr Thr Val Leu Phe Asn Glu Arg Ala Thr 35 40 45

Thr Asn Phe Gly Gln Asn Val His Leu Thr Gly Ser Ile Ser Gln Leu 50 60

Gly Ser Trp Asp Thr Asp Ser Ala Val Ala Leu Ser Ala Val Asn Tyr 65 70 75 80

Thr Ser Ser Asp Pro Leu Trp Phe Val Arg Val Gln Leu Pro Ala Gly 85 90 95

Thr Ser Phe Gln Tyr Lys Tyr Phe Lys Lys Asp Ser Ser Asn Ala Val 100 105 110

Ala Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Leu Asn Cys 115 120 125

Ala Gly Thr Ala Thr Glu Asn Asp Thr Trp Arg 130 135

<210> 23

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<212> PRT

<213> Eupenicillium ludwigii

<220>

<221> MISC FEATURE

<222> (1)..(126)

<223> CBM

<400> 23

Ser Thr Thr Thr Ser Thr Thr Lys Thr Thr Thr Thr Ser Thr Thr 1 5 10 15

Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Ile 20 25 30

Ala Thr Thr Tyr Tyr Gly Glu Asn Ile Lys Ile Ala Gly Ser Ile Ser 35 40 45

Gln Leu Gly Asp Trp Asp Thr Ser Asn Ala Val Ala Leu Ser Ala Ala 50 55 60

Asp Tyr Thr Ser Ser Asp His Leu Trp Phe Val Asp Ile Asp Leu Pro 75 80

Ala Gly Thr Val Phe Glu Tyr Lys Tyr Ile Arg Ile Glu Ser Asp Gly 85 90 95

Ser Ile Glu Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala 100 105 110

Ala Cys Ala Thr Thr Ala Val Thr Glu Asn Asp Thr Trp Arg 115 120 125

<210> 24

<211> 116

<212> PRT

<213> Aspergillus japonicus

<220>

<221> MISC_FEATURE

<222> (1)..(116)

<223> CBM

<400> 24

Lys Thr Ser Thr Thr Thr Ser Ser Cys Ser Thr Pro Thr Ser Val Ala 1 5 10 15

Val Thr Phe Asp Val Ile Ala Thr Thr Thr Tyr Gly Glu Asn Val Tyr

Ile Ser Gly Ser Ile Ser Gln Leu Gly Ser Trp Asp Thr Ser Ser Ala

Ile Ala Leu Ser Ala Ser Gln Tyr Thr Ser Ser Asn Asn Leu Trp Tyr
50 55 60

Ala Thr Val His Leu Pro Ala Gly Thr Thr Phe Gln Tyr Lys Tyr Ile
65 70 75 80

Arg Lys Glu Thr Asp Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg 85 90 95

Ser Tyr Thr Val Pro Ser Ser Cys Gly Val Ser Ser Ala Thr Glu Ser 100 105 110

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Asp Thr Trp Arg
      115
<210> 25
<211> 133
<212> PRT
<213> Penicillium cf. miczynskii
<220>
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<223> CBM
<400> 25
Thr Thr Thr Gly Gly Thr Thr Thr Ser Gln Gly Ser Thr Thr Thr Thr
                          10 15
Ser Lys Thr Ser Thr Thr Ser Ser Cys Thr Ala Pro Thr Ser Val
Ala Val Thr Phe Asp Leu Ile Ala Thr Thr Val Tyr Asp Glu Asn Val
Gln Leu Ala Gly Ser Ile Ser Ala Leu Gly Ser Trp Asp Thr Ser Ser
 50 55 60
Ala Ile Arg Leu Ser Ala Ser Gln Tyr Thr Ser Ser Asn His Leu Trp
                   70
Tyr Val Ala Val Ser Leu Pro Ala Gly Gln Val Phe Gln Tyr Lys Tyr
 Ile Arg Val Ala Ser Ser Gly Thr Ile Thr Trp Glu Ser Asp Pro Asn
            100 105
 Leu Ser Tyr Thr Val Pro Val Ala Cys Ala Ala Thr Ala Val Thr Ile
                                             125
        115
 Ser Asp Thr Trp Arg
   130
 <210> 26
<211> 116
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<212> PRT

<213> Mzl Penicillium sp.

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Leu Val Gly Ser Ile Ser Glu Leu Gly Asp Trp Asp Thr Gly Ser Ala 35 40 45

Ile Ala Leu His Ala Thr Asp Tyr Thr Asp Ser Asp His Leu Trp Phe 50 55 60

Val Thr Val Gly Leu Pro Ala Gly Ala Ser Phe Glu Tyr Lys Tyr Ile 65 70 75 80

Arg Val Glu Ser Ser Gly Thr Ile Glu Trp Glu Ser Asp Pro Asn Arg 85 90 95

Ser Tyr Thr Val Pro Ala Ala Cys Ala Thr Thr Ala Val Thr Glu Ser 100 105 110

Asp Thr

<210> 28

<211> 111

<212> PRT

<213> Humicola grisea var. thermoidea

<220>

<221> MISC_FEATURE

<222> (1)..(111)

<223> CBM

<400> 28

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Ala Trp Gly Glu Thr Ile Lys Val Val Gly Asn Val Pro Ala Leu Gly 20 25 30

Asn Trp Asp Thr Ser Lys Ala Val Thr Leu Ser Ala Ser Gly Tyr Lys
35 40 45

Ser Asn Asp Pro Leu Trp Ser Ile Thr Val Pro Ile Lys Ala Thr Gly
50 55 60

Ser Ala Val Gln Tyr Lys Tyr Ile Lys Val Gly Thr Asn Gly Lys Ile 65 70 75 80

Thr Trp Glu Ser Asp Pro Asn Arg Ser Ile Thr Leu Gln Thr Ala Ser 85 . 90 95

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           100 105
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<211> 108
<212> PRT
<213> Aspergillus niger
<220>
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<223> CBM
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Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu
                              25
           20
Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr
                   40
Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly
                       55
Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val
65
Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys
                                   90
Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
            100
<210> 30
<211> 97
<212> PRT
<213> Athelia rolfsii
<220>
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Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr 35 40 45

Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile 50 55 60

Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile 65 70 75 80

Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu 85 90 95

Ser

<210> 31

<211> 640

<212> PRT

<213> Aspergillus kawachi alpha-amylase

<220>

<221> mat_peptide

<222> (22)..(640)

<400> 31

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-5 -1 1 5 10

Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr 15 20 25

Ala Thr Cys Asn Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln 30 35

Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala 45 50 55

- Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ser Asp 60 65 70 75
- Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Tyr Val Asn 80 85 90
- Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu 95 100 105
- His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
- Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
- Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp 140 145 150 150
- Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val 160 165 170
- Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp 175 180 185
- Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu 190 195 200
- Arg Ile Asp Ser Val Glu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr 205 210 215
- Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn 220 225 230 230
- Pro Ala Leu Asp Cys Pro Tyr Gln Lys Tyr Leu Asp Gly Val Leu Asn 240 245 250
- Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Gly 255 260 265
- Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys 270 275 280
- Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro 285 290 295

Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu 300 305 310 315

- Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu 320 325 330
- Glu Gln His Tyr Ser Gly Gly Asp Val Pro Tyr Asn Arg Glu Ala Thr 335 340 345
- Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala 350 355 360
- Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Asp Tyr 365 370 375
- Ile Thr Tyr Lys Asn Asp Pro Ile Tyr Thr Asp Ser Asn Thr Ile Ala 380 385 390 395
- Met Arg Lys Gly Thr Ser Gly Ser Gln Ile Ile Thr Val Leu Ser Asn 400 405 410
- Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly 415 420 425
- Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val 430 435 440
- Thr Val Asp Ser Asn Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu 445 450 455
- Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys 460 465 470 475
- Gly Gly Ser Gly Asn Thr Thr Thr Thr Thr Thr Ala Ala Thr Ser Thr
 480 485 490
- Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala Thr Thr 495 500 505
- Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu 510 515 520
- Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser 525 530 535

Ile 540	Ser	Gln	Leu	Gly	Glu 545	Trp	His	Thr	Ser	: As 55	p A] 0	la V	al	Lys	Le	u S . 5	er 55	
Ala	Asp	Asp	Tyr	Thr 560	Ser	Ser	Asn	Pro	Glu 565	ı Tr	p Se	er V	/al	Thr	Va 57	11 S '0	er	
Leu	Pro	Val	Gly 575	Thr	Thr	. Phe	g Glu	1 Ty1 580	. Ly:	s Ph	ne I	le ^l	ГÀЗ	Val 585	As	sp G	Slu	
Gly	Gly	Ser 590	Val	Thi	r Trp	Glu	sei 59!	c Ası	p Pr	o As	sn A	rg (G1u 600	Tyr	Tł	ar V	/al	
Pro	Glu 605	Cys	G13	, Sei	r Gl	y Se: 61	r Gl;	y Gl	u Th	r V	al V 6	al . 515	Asp	Thr	T	rp i	Arg	
		32 1860 DNA Arti		ial							٠							
	20> 23>	+-	. 7 +	icd	omai	n-As	perq	perg jillu er gl	12 1/4	awac	J	~		alp)	na- las	·amy ie	lase	
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	at cg sp Ar	g tt	c gg le Gi	TA W	gg a rg T	cg g hr A	ac a sp A	311 0	cg a er T 5	icg 'hr	aca Thr	gct Ala	ac Th	a to r Cy 30) (s	gat Asp	acg Thr	96
g: G:	gt ga ly As	ac ca sp Gl	ln I	tc t le T	at t yr C	gt g ys G	TA G	gc a ly S 0	gt t er 7	gg Trp	caa Gln	GJ?	a at 7 Il 45	c at e I.	c Le	aac Asn	cat His	144
r c.	tg ga eu Aa	at ta		tc c	ag g Sln G	iŤλ κ	tg g let 6	ga t Sly E	tc a	acg Thr	gcc Ala	ato 110 60	e tg	g a	tc le	tcg	cct Pro	192
a	_ ,																	

gga Gly	tat Tyr	tgg Trp	cag Gln	cag Gln 85	aag Lys	ata Ile	tac Tyr	gac Asp	gtg Val 90	aac Asn	tcc Ser	aac Asn	ttc Phe	ggc Gly 95	act Thr	288
gca Ala	gat Asp	gac Asp	ctc Leu 100	aag Lys	tcc Ser	ctc Leu	tca Ser	gat Asp 105	gcg Ala	ctt Leu	cat His	gcc Ala	cgc Arg 110	gga Gly	atg Met	336
tac Tyr	ctc Leu	atg Met 115	gtg Val	gac Asp	gtc Val	gtc Val	cct Pro 120	aac Asn	cac His	atg Met	ggc	tac Tyr 125	gcc Ala	ggc Gly	aac Asn	384
ggc Gly	aac Asn 130	gat Asp	gta Val	gac Asp	tac Tyr	agc Ser 135	gtc Val	ttc Phe	gac Asp	ccc Pro	ttc Phe 140	gat Asp	tcc Ser	tcc Ser	tcc Ser	432
Tyr 145	Phe	His	Pro	Tyr	Cys 150	Leu	ITE	aca Thr	Asp	155	Asp	ASII	пси		160	480
Val	Gln	Asp	Cys	Trp 165	GIU	стХ	Asp	TIIL	170	Vair	÷			175		528
Asn	Thr	Thr	Glu 180	Thr	Ala	Val	Arg	aca Thr 185	116	iip	- Y -	пор	190			576
Asp	Leu	Val 195	Ser	Asn	Tyr	Ser	200		ету	ъеа	nry	205				624
Leu	Glu 210	Val	. Glu	l Pro	Asp	215	Pne	PIO	GIY	TÄT	220)			ggt Gly	672
Val 225	Tyr	Cys	s Val	- Gly	230	. vaı	Asp) ASI	. GI	235	, , ,	,		-	tgc Cys 240	720
Pro	Туг	Glı	а Буз	245	Leu	Asp	GT?	y vai	250)	y.			255		768
Gln	Let	ı Le	и Ту: 26	r Ala	. Phe	e Git	i Sei	265	, 261	. 613	y be.		270)	ctc Leu	816
Туг	Ası	n Me 27	t Il 5	е Lys	s Sei	: Val	280 280	a Sei	C AS	, cys	, DC.	28	5		a cta r Leu	864
Lev	29)	y As O	n Ph	e Il	e GII	29!	1 H1:	s Asj	p As	11 11	30	0			c tac r Tyr	912
acc Thi	r Se	c ga r As	c ta p Ty	c tc r Se	g caa r Gl: 31	U AT	c aa a Ly	a aa s As:	c gt n Va	c cte l Le 31	<u>.</u>	c ta r Ty	c at r Il	c tt e Ph	c ctc e Leu 320	

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Ser	Ser	Tyr	Thr 420	Leu	Thr	Leu	Ser	Gly 425	Ser	GTĀ	Tyr	aca Thr	430	GTĀ	1111	1296
Lys	Leu	Ile 435	Glu	Ala	Tyr	Thr	Cys 440	Thr	Ser	vaı	THE	gtg Val 445	кър	261	DCI	1344
Gly	Asp 450	Ile	Pro	Val	Pro	Met 455	Ala	Ser	GTÀ	Leu	460	aga Arg	val	neu	пец	1392
Pro 465	Ala	Ser	Val	Val	Asp 470	Ser	Ser	Ser	Leu	Cys 475	GTĀ	GJ À aaa	ser	СТУ	480	1440
Thr	Thr	Thr	Thr	Thr 485	Thr	Ala	Ala	ALA	490	Ser	THE	tcc Ser	пуз	495	1,111	1488
Thr	Ser	Ser	Ser 500	Ser	Ser	Ser	Ala	505	i Ala	Thr	THE	tct Ser	510	Ser	Cys	1536
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Thr	Tyr 530	· Gly	/ Glu	Asn	. Ile	535	Leu ,	ı Val	L GI	, Ser	540	e Ser	. GII	тес	ggt	1632
gad Asp 545	Trp	gaa Glu	a acc	ago Ser	gac Asp 550	Gl3	ata Ile	a gct e Ala	cto a Lev	g agt ser 555	: Ala	gac Asp	aaq Lys	tac Tyr	thr 560	1680

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G17	Asp	Gln 35	Ile	Tyr	Суз	Gly	Gly 40	Ser	Trp	Gln	Gly	Ile 45	Ile	Asn	His		
Let	i Asp 50	Tyr	Ile	Gln	Gly	Met 55	Gly	Phe	Thr	Ala	Ile 60	Trp	Ile	Ser	Pro		
Ile 65	e Thr	Glu	. Gln	Leu	Pro	Gln	Asp	Thr	Ala	Asp 75	Gly	Glu	Ala	Tyr	His 80		
Gl	, Tyr	Trp	Gln	Gln 85	Lys	Ile	Туг	Asp	Val 90	Asn	Ser	Asn	Phe	Gly 95	Thr	•	
Ala	a Asp	Asp	Leu 100		Ser	Leu	Ser	Asp 105	Ala	Leu	His	Ala	Arg	Gly	Met		
Тy	c Leu	1 Met		Asp	Val	Val	Pro 120		His	Met	Gly	Tyr 125	Ala	Gly	Asn		

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- Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met 145 150 155 160
- Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175
- Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190
- Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205
- Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly 210 215 220
- Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys 225 230 230 235
- Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp 245 250 255
- Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu 260 265 270
- Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285
- Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300
- Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315
- Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser 325 330 335
- Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350
- Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile 355 360 365

- Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380
- Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr 385 390 395
- Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405 410
- Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr 420 425 430
- Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser 435
- Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu 450 455 460
- Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg 465 470 475 480
- Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr 485 490 495
- Thr Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys 500 505
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- Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly 530 535
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- Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu 565 570 575
- Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu 580 585 590
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ccc Pro 465	gcg Ala	tcc Ser	gtc Val	gtc Val	gat Asp 470	agc Ser	tct Ser	tcg Ser	ctc Leu	tgt Cys 475	ggc Gly	Gly ggg	agc Ser	gga Gly	aga Arg 480	1440
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Thr	Ser	Ser	Ser 500	Ser	Ser	Ser	Ala	505	АТА	act Thr	1111	Jei.	510	502		1536
Glu	Val	Thr 515	Phe	Asp	Val	Tyr	520	Thr	Tnr	gta Val	тĀт	525	GIII	,	110	1584
Tyr	530	Thr	Gly	Asp	Val	535	GIO	Leu	. Сту	ASII	540)		• • • • • • • • • • • • • • • • • • • •	aat Asn	1632
Gl ₃ 545	v Val	. Ala	Leu	Ser	550) : Ala	AST	ı Tyr	PIC	555	111	, 501	1124		atc : Ile 560	1680
Ala	. Lev	ı Pro) Ala	Asp 565	Thr	Thr	: Ile	e GIr	570) . rĀs	, туг	. 441	. noi.	575		1728
Gly	y Sei	Th	val 580	L Il∈	e Trp	GIV	ı Ası	585	5	s ser	. ASI	ı ALÇ	590) .	acg Thr	1776
ac ₍ Th:	g cco	gco Ala 59	a Sei	c Gly	c aca	a tao	c acc c Th:	r GII	a aaa 1 Lys	a gad s Asi	c act	t tgg r Tr 60!) Mar	gaa Glu	a tct ı Ser	1824
ta	g															1827

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Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His 35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro 50 55 60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His 65 70 75 80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr 85 90 95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met 100 105 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn 115 120 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser 130 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met 145 150 155 160

Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly 210 215 220

- Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys 225 230 230 235
- Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp 245 250 255
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- Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285
- Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300
- Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315
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- Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380
- Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400
- Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405 410
- Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
- Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
- Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu 450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg 475 470 465 Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr 485 Thr Ser Ser Ser Ser Ser Ala Ala Thr Thr Ser Ser Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile 525 520 515 Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn 540 535 530 Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile 550 -545 Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp 570 565 Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr 585 580 Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser 600 595 <210> 36 <211> 1863 <212> DNA <213> Artificial <220> Hybrid consisting of A.oryzae alpha-amylase catalytic domain-A. <223> kawachii alpha-amylase linker-A. kawachi alpha-amylase CBD <220> <221> CDS (1)..(1863) <222> <223> Hybrid <400> 36 gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc ctt ctc acg 48 Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr 10

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gcg Ala	gat Asp	cag Gln 35	aaa Lys	tac Tyr	tgt Cys	ggt Gly	gga Gly 40	aca Thr	tgg Trp	cag Gln	ggc Gly	atc Ile 45	atc Ile	gac Asp	aag Lys	144
ttg Leu	gac Asp 50	tat Tyr	atc Ile	cag Gln	gga Gly	atg Met 55	ggc Gly	ttc Phe	aca Thr	gcc Ala	atc Ile 60	tgg Trp	atc Ile	acc Thr	ccc Pro	192
gtt Val 65	aca Thr	gcc Ala	cag Gln	ctg Leu	ccc Pro 70	cag Gln	acc Thr	acc Thr	gca Ala	tat Tyr 75	gga Gly	gat Asp	gcc Ala	tac Tyr	cat His 80	240
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ggt Gly	agc Ser 130	Ser	gtc Val	gat Asp	tac Tyr	agt Ser 135	gtg Val	ttt	aaa Lys	ccg Pro	ttc Phe 140	Ser	tcc Ser	caa Gln	gac Asp	432
tac Tyr 145	Phe	cac His	ccg Pro	ttc Phe	tgt Cys 150	Phe	att Ile	caa Gln	aac Asn	tat Tyr 155	GIU	gat Asp	cag Gln	act Thr	cag Gln 160	480
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gat Asp	acc Thr	acc Thr	aag Lys 180	Asp	gtg Val	gtc Val	aag Lys	aat Asn 185	GIU	tgg Trp	tac Tyr	gac Asp	tgg Trp 190	, , ,,,,	gga Gly	576
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aaa Lys	a cad s His 210	va.	c caç l Glr	g aag n Lys	g gad s Asp	tto Phe 215	Trp	g ccc Pro	. GJ7	tac Tyr	Ası 220	ı mă:	gco Ala	gca Ala	a ggc a Gly	672
gte Vai 22	l Ty	c tg	t ato	e Gly	gaç Glu 230	ı Val	g cto L Lev	gac 1 Asp	ggt Gly	gat Asr 235) ET	g gco o Ala	tac Tyr	e act	tgt Cys 240	720
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Gly	Gly	Asn	Asp 340	Pro	Ala	Asn	Arg	gaa Glu 345	Ala	Tnr	тър	теп	350		ıyı.	1056
Pro	Thr	Asp 355	Ser	Glu	Leu	Tyr	Lys 360	tta Leu	IIe	Ala	ser	365	ASII	ИТĠ	116	1104
Arg	Asn 370	Tyr	Ala	Ile	Ser	Lys 375	Asp	aca Thr	GTA	Phe	380	Inr	туг	пўз	ASII	1152
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Asp	Ser	Tyr	Thr 420	Leu	Ser	Leu	Ser	Gly 425	Ala	GIA	туг	Thr	430	СТУ	cag Gln	1296
Gln	Leu	435	Glu	Val	Ile	Gly	440	Thr	Thr	· vai	. Thi	445	GTĀ	361	gat Asp	1344
Gly	450	Val	. Pro	Val	. Pro	Met 455	Ala	. Gly	. GTĀ	, rer	460)	, val	. пес	tat Tyr	1392
Pro 465	Thr	Glu	ı Lys	Lev	470	Gly	Ser	Lys	: ITE	475	s Sei	r Sei	Ser	. Gry	aga Arg 480	1440
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gga gag tgg gat acg agt gac gcg gtg aag ttg tcc gcg gat gat Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp 545 550	tat 1680 Tyr 560
acc tcg agt aac ccc gag tgg tct gtt act gtg tcg ttg ccg gtg Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val 565 570 575	ggg 1728 Gly
acg acc ttc gag tat aag ttt att aag gtc gat gag ggt gga agt Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser 580 585	gtg 1776 Val
act tgg gaa agt gat ccg aat agg gag tat act gtg cct gaa tgt Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys 595 600 605	ggg 1824 Gly
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<220> <223> Synthetic Construct	
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Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile T 50 55 60	hr Pro

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His 65 70 75 80

- Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr 85 90 95
- Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
 100 105 110
- Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala 115 120 125
- Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp 130 135 140
- Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln 145 150 155 160
- Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu 165 170 175
- Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly 180 185 190
- Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val 195 200 205
- Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly 210 215 220
- Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys 225 230 235 240
- Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr 245 250 255
- Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu 260 265 270
- Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu 275 280 285
- Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu 305 310 315 320

- Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala 325 330 335
- Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350
- Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile 355 360 365
- Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn 370 375
- Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400
- Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly 405 410 415
- Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln 420 430
- Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp 435 440 445
- Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr 450 455 460
- Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg 465 470 480
- Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr 485 490 495
- Thr Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys 500 505
- Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu Glu Leu Val Thr 515 520 525
- Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser Ile Ser Gln Leu 530 535

Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr 545 Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val Gly 570 Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser Val 590 585 Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly 600 Asn Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg 615 <210> 38 1767 <211> ĎΝΆ <212> <213> Artificial <220> Hybrid consisting of A. niger acid alpha-amylase catalytic <223> domain- A.rolfsii glucoamylase linker- A. rolfsii glucoamylase <220> <221> CDS (1)..(1767)<222> <223> Hybrid <400> 38 ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg 48 Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr 10 gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg 96 Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr .25 ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat 144 Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His 40 ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct 192 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat 240 Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His

gga Gly	tat Tyr	tgg Trp	cag Gln	cag Gln 85	aag Lys	ata Ile	tac Tyr	Asp	gtg Val 90	aac Asn	tcc Ser	aac Asn	ttc Phe	ggc Gly 95	act Thr	288
gca Ala	gat Asp	gac Asp	ctc Leu 100	aag Lys	tcc Ser	ctc Leu	tca Ser	gat Asp 105	Ala	ctt Leu	cat His	gcc Ala	cgc Arg 110	gga Gly	atg Met	 336
tac Tyr	ctc Leu	atg Met 115	gtg Val	gac Asp	gtc Val	gtc Val	cct Pro 120	aac Asn	cac His	atg Met	ggc Gly	tac Tyr 125	gcc Ala	ggc Gly	aac Asn	384
ggc	aac Asn 130	Asp	gta Val	gac Asp	tac Tyr	agc Ser 135	gtc Val	ttc Phe	gac Asp	ccc Pro	ttc Phe 140	gat Asp	tcc Ser	tcc Ser	tcc Ser	432
tac Tyr 145	Phe	cac His	cca Pro	tac Tyr	tgc Cys 150	ctg Leu	atc Ile	aca Thr	gat Asp	tgg Trp 155	gac Asp	aac Asn	ttg Leu	acc Thr	atg Met 160	480
gto Val	caa Gln	gat Asp	tgt Cys	tgg Trp 165	gag Glu	ggt Gly	gac Asp	acc Thr	atc Ile 170	gta Val	tct Ser	ctg Leu	cca Pro	gac Asp 175	cta Leu	528
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ga Ası	c cto p Lev	gta Val	L Ser	aat Asn	tat Tyr	tca Ser	gtc Val 200	ASP	gga Gly	ctc Leu	cgc	ato Ile 205		agt Ser	gtc Val	624
ct: Le:	c gaa u Glu 210	ı Val	gaa L Glu	a cca ı Pro	gac Asp	ttc Phe 215	Pne	ccg Pro	ggc Gly	tac Tyr	cag Glr 220		gca Ala	gca Ala	ggt	672
gt Va 22	l Ty:	c tgo	c gto s Vai	c ggo	gaa Glu 230	ı vaı	gac Asp	aac Asn	ggc	aac Asr 235		gco Ala	cto Lev	gac Asp	tgc Cys 240	720
cc Pr	a ta o Ty	c ca r Gl	g aa n Ly	g gto s Val 24!	г гел	g gac ı Asp	ggc Gly	gto Val	cto Lev 250		tai	t cco	g ato	tac Type 255	tgg Trp	768
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ta T <u>y</u>	ıc aa vr As	c at n Me 27	t Il	c aa e Ly	a tc s Se:	c gto r Vai	c gca l Ala 280	a ser	ga As	c tg p Cy	c tc s Se	c ga r As 28		g ac	a cta r Leu	864
ct Le	c gg eu Gl 29	y As	ic tt in Ph	c at e Il	c ga e Gl	a aa u As: 29	u Hl	c gad s Asp	c aa o As	t cc n Pr	c cg o Ar 30	9	c gc e Al	c tc a Se	c tac r Tyr	912
T	cc to hr Se	ec ga er As	ac ta sp Ty	ıc to /r Se	g ca r Gl	n Al	c aa a Ly	a aa s Asi	c gt n Va	c ct l Le 31		ıc ta er Ty	c at r Il	c tt e Ph	c ctc e Leu 320	960

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Arg	Lys 370	Leu	Ala	Ile	Ser	Ala 375	Asp	Ser	Ата	tac Tyr	380	IIIT	ŢŸĽ	ALG	ASII	1152
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ggt Gl	gct Ala	aca Thi	a ago	e ccg Pro 485) GTA	ggc Gly	tco Ser	tco Ser	g ggt Gly 490	261	gto Val	gag Glu	gto Val	act Thr 495	ttc Phe	1488
gad Ası	gtt Val	tae L Ty:	c gct r Ala 500	1 Thi	aca Thr	a gta : Val	a tat L Ty:	ggc Gl ₃ 505	, GT1	g aac n Asr	ato 11e	tat Tyr	: ato : Ile 510		ggt Gly	1536
gai As _l	t gto o Va	g ag L Se 51	r Glı	g cto 1 Le	gg¢ ıGly	c aad y Asi	tgg n Trj 520) III	a cco	c gcc	a aat	ggt n Gly 525		gca L Ala	a ctc a Leu	1584
tc Se	t tc r Se 53	r Al	t aa a As:	c tac n Ty:	c ccc	c according to the contract of	r Tr	g ag p Se:	t gce r Ala	c acq a Thi	g ate r Ile 54		t cto a Leo	e cc	c gct o Ala	1632

gac acg aca atc cag tac aag tat gtc aac att gac ggc agc acc gtc 1680 Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val 555 550 545 atc tgg gag gat gct atc agc aat cgc gag atc acg acg ccc gcc agc 1728 Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser 570 565 1767 ggc aca tac acc gaa aaa gac act tgg gat gaa tct tag Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser <210> 39 <211> 588 <212> PRT <213> Artificial <220> <223> Synthetic Construct <400> 39 Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr 30 Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His 40 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro 50 Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr 90 85 Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met 105 100 Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn 120 Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser 135

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met 145 150 155 160

- Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu 165 170 175
- Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala 180 185 190
- Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val 195 200 205
- Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly 210 215 220
- Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys 225 230 235 240
- Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
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- Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu 260 265 270
- Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu 275 280 285
- Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300
- Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu 305 310 315
- Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser 325 330 335
- Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350
- Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile 355 360 365
- Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn 370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr 395 390

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly 405

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr 430 425 420

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser 440 435

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu 450

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg 470 465

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe 490 485

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Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu 520

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala 540 535 530

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DNA <212>

<213> Artificial

<220>

Hybrid containing A. oryzae alpha-amylase catalytic domain- A. <223> rolfsii glucoamylase linker- A. rolfsii glucoamylase CBM

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gcg Ala	gat Asp	cag Gln 35	aaa Lys	tac Tyr	tgt Cys	ggt Gly	gga Gly 40	aca Thr	tgg Trp	cag Gln	ggc Gly	atc Ile 45	atc Ile	gac Asp	aag Lys	;	144
ttg Leu	gac Asp 50	tat Tyr	atc Ile	cag Gln	gga Gly	atg Met 55	ggc Gly	ttc Phe	aca Thr	gcc Ala	atc Ile 60	tgg Trp	atc Ile	acc Thr	ccc Pro		192
gtt Val 65	aca Thr	gcc Ala	cag Gln	ctg Leu	ccc Pro 70	cag Gln	acc Thr	acc Thr	gca Ala	tat Tyr 75	gga Gly	gat Asp	gcc Ala	tac Tyr	cat His 80		240
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gca Ala	gat Asp	gac Asp	ttg Leu 100	aag Lys	gcg Ala	ctc Leu	tct Ser	tcg Ser 105	gcc Ala	ctt Leu	cat His	gag Glu	agg Arg 110	Gly	atg Met		336
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tac Tyr 145	Phe	cac His	Pro	Phe	Cvs	Phe	Ile	caa Gln	Asn	tat Tyr 155	GIU	gat Asp	cag Gln	act Thr	cag Gln 160		480
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Lys	His 210	Val	Gln	Lys	Asp	Phe 215	Trp	Pro	СТÀ	Tyr	220	пуз	gcc Ala	AIG	Gry	672
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cca Pro	ctc Leu	ctc Leu	aac Asn 260	gcc Ala	ttc Phe	aag Lys	tca Ser	acc Thr 265	tcc Ser	ggc Gly	agc Ser	atg Met	gac Asp 270	gac Asp	ctc Leu	816
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gat Ası	t tco	g ta r Ty	t acc r Th: 42	r Leu	c tco ı Sei	c tto	g agt ı Se:	t gg r Gl; 42	A WT	g gg	t ta y Ty	c ac r Th	a gco r Ala 430		c cag y Gln	1296
ca: Gl:	a tte	g ac u Th 43	r Gl	g gte u Vai	c ati	t gg e Gl	c tg y Cy 44	s m	g ac r Th	c gt r Va	g ac l Th	g gt r Va 44	T 0-	t tc y Se	g gat r Asp	1344

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ccg Pro 465	act Thr	gag Glu	aag Lys	ttg Leu	gca Ala 470	ggt Gly	agc Ser	aag Lys	atc Ile	tgt Cys 475	agt Ser	agc Ser	tcg Ser	gga Gly	aga Arg 480	1440
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gat Asp	gtg Val	agt Ser 515	Glu	ctc Leu	ggc Gly	aac Asn	tgg Trp 520	aca Thr	ccc Pro	gcc Ala	aat Asn	ggt Gly 525	gtt Val	gca Ala	ctc Leu	1584
tct Sei	tct Ser 530	Ala	aac Asn	tac Tyr	ccc Pro	acc Thr 535	Trb	agt Ser	gcc Ala	acg Thr	atc Ile 540		ctc Leu	ccc Pro	gct Ala	1632
gad Asj	Thr	aca Thr	ato : Ile	cag Gln	tac Tyr 550	гАг	tat Tyr	gtc Val	aac Asn	att Ile 555		ggc	agc Ser	acc Thr	gtc Val 560	1680
ate Il	c tgg e Trp	g gag o Glu	g gat ı Asp	gct Ala 565	ITe	ago Ser	aat Asr	. cgc	gag Glu 570	1 110	acg Thr	acg Thr	p ccc Pro	gcc Ala 575	agc Ser	1728
gg Gl	c aca y Thi	a tao	c acc r Thi	r Gli	a aaa 1 Lys	a gad s Asp	act Thi	tgg Tri 1585) Wor	gaa Glu	tct Sei	tag		·		1767
<2 <2	10> 11> 12> 13>	41 588 PRT Art	ific	ial											ŧ	
	20>	Syn	thet	ic C	onst:	ruct							•			
	.00> .a Th		o Al	a As 5	p Tr	p Ar	g Se	r Gl	n Se 10	r Il	е Ту	r Ph	e Le	u Le 15	u Thr	
A	sp Ar	g Ph	ne Al 20		g Th	r As	p Gl	у Se 25	r Th	r Th	r Al	a Th	r Cy 30	s As	n Thr	·

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys 35

- Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro 50 55 60
- Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His 70 75 80
- Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr 85 90 95
- Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met 100 105 110
- Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala 115 120 125
- Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
- Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln 145 150 155 160
- Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu 165 170 175
- Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly 180 185
- Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
- Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
- Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys 225 230 235
- Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr 245 250 255
- Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu 260 265
- Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu 275 280 285

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr 290 295 300

- Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu 305 310 315 320
- Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala 325 330 335
- Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr 340 345 350
- Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile 355 360 365
- Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn 370 375 380
- Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr 385 390 395 400
- Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly 405 410 415
- Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln 420 425 430
- Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp 435 440 . 445
- Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr 450 455 460
- Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg 465 470 480
- Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
 485 490 495
- Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly 500 505 510
- Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu 515 520 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala 530 535 540

Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val 545 550 555 560

Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser565570

Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser 580 585